

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: US/09/676,249D
Source: IFW/6
Date Processed by STIC: 10-26-04

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 10/26/2004

PATENT APPLICATION: US/09/676,249D

TIME: 16:00:00

Input Set : A:\3153.162.PC10555A.Second.Substitute.Seq.10.19.04.ST25.txt

Output Set : N:\CRF4\10262004\I676249D.raw

3 <110> APPLICANT: Pfizer, Inc. and Pfizer Products, Inc.
 5 <120> TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA HYOPNEUMONIAE

nbp3

6 GENE AND USES THEREOF
 8 <130> FILE REFERENCE: 3153.00162/PC10555
 10 <140> CURRENT APPLICATION NUMBER: US 09/676,249D
 11 <141> CURRENT FILING DATE: 2000-09-29
 13 <150> PRIOR APPLICATION NUMBER: US Prov. 60/156,602
 14 <151> PRIOR FILING DATE: 1999-09-29
 16 <160> NUMBER OF SEQ ID NOS: 42
 18 <170> SOFTWARE: PatentIn version 3.2
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1692
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Mycoplasma hyopneumoniae
 25 <400> SEQUENCE: 1

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28	tcacgtaat	taaaacaatt	aattaggaga	acaactatga	aaaaaaagat	aaaatgaaat	120
30	aaatttcttg	gcttaggctt	agtttttccg	ctttcagcaa	tcgcgacaat	ctctgccgga	180
32	tgttgggata	aagaaacaac	taaagaagaa	aatcagcccg	ataatcaaaa	taagcaaatac	240
34	actgatgtct	caaaaatttc	aggactagtt	aatgaacgaa	aatccgaaat	tatggccgca	300
36	aaagctgatg	caaacaaaca	ttttgggcta	aatatggcaa	ttgtaaccgc	tggtggaacg	360
38	gtaaatgata	attcatttaa	ccaatcaagt	tgagaggcaa	ttcaacaact	tggegtctct	420
40	actggagggtg	agattacttc	agtagatagt	tcaactgctg	aacttgaagg	aaaatatagc	480
42	tcacttgcta	ataccaacaa	aaatgtttga	gtactttctg	gttttcaaca	cggtgatgcg	540
44	ttcacaaagt	gattaaaaat	ccctgaaaat	aagcaattat	ttactgaaaa	aaatattatc	600
46	atactcggaa	ttgactgaac	tgatactgaa	aatgtaattc	caacaggctg	atatattaat	660
48	ttaacctata	aaactgaaga	agccggatga	cttgaggat	atgcgaatgc	ttcctttttg	720
50	gcaaaaaaat	tcccaagtga	tccaactaaa	agatcagcaa	ttgttatcgg	tggtgggatt	780
52	tcgccagctg	taactgattt	tatcgctggg	tatctagccg	gaattaaagc	ttgaaatcta	840
54	aaaaattctg	ataaaaaaac	aaagataaca	actgataaaa	tcgagataaa	tcttgggttt	900
56	gatgttcaag	atacttcaac	aaaagaaaga	cttgaacaaa	ttgcttcaaa	agataaacct	960
58	tcaacactat	tagctgtcgc	tggaaccact	actgaaattt	tctcggatat	aatcgcaaac	1020
60	caaatgatc	gttatctcat	tggtgttgac	accgaccaat	cacttgttta	tacaaaaact	1080
62	aaaaataaat	ttttcacctc	aattttgaaa	aatttaggtt	actccgtttt	cagcgttctt	1140
64	agtgatttat	ataccaaaaa	atcaaattca	agaaatttag	ccggctttga	atttggtaaa	1200
66	aaaagtgcaa	ccgtttatct	tggaattaaa	gacaggtttg	tcgatattgc	tgatacttct	1260
68	ttagaaggca	atgataaaaa	actcgcaact	gaagccattt	ctgaagctaa	aaaagaattt	1320
70	gaagaaaaaa	ctaagacaat	tcctgccgaa	gaagtccgta	aaactttaga	aattccggaa	1380
72	atgcctgata	aacaacctga	taagcaacag	gaaagcttag	acaaactaat	taccgatatt	1440
74	aataaaaaat	aagtaagaaa	aaataacaat	tttttaacat	tatatctttt	tttagagatt	1500
76	aattttcttc	taatttagtt	taatttaata	taaaattata	ttaaattaaa	aaaataaaaa	1560
78	atccggacta	tttttgttcc	ggatttttta	tttttggtt	actatttaat	ataatgataa	1620
80	atcaggatta	tgcaattgaa	tttattcaag	tctcgaaaaa	atttggcagt	ttttatgcca	1680

(pg. 6)

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Input Set : A:\3153.162.PC10555A.Second.Substitute.Seq.10.19.04.ST25.txt

Output Set: N:\CRF4\10262004\I676249D.raw

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86 <211> LENGTH: 451
87 <212> TYPE: PRT
88 <213> ORGANISM: Mycoplasma hyopneumoniae
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96 Phe Pro Leu Ser Ala Ile Ala Thr Ile Ser Ala Gly Cys Trp Asp Lys
97          20          25          30
100 Glu Thr Thr Lys Glu Glu Lys Ser Ala Asp Asn Gln Asn Lys Gln Ile
101          35          40          45
104 Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu Arg Lys Ser Glu
105          50          55          60
108 Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe Gly Leu Asn Met
109 65          70          75          80
112 Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn Ser Phe Asn Gln
113          85          90          95
116 Ser Ser Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu Thr Gly Gly Glu
117          100         105         110
120 Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu Gly Lys Tyr Ser
121          115         120         125
124 Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu Ser Gly Phe Gln
125          130         135         140
128 His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro Glu Asn Lys Gln
129 145          150         155         160
132 Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile Asp Trp Thr Asp
133          165         170         175
136 Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn Leu Thr Tyr Lys
137          180         185         190
140 Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn Ala Ser Phe Leu
141          195         200         205
144 Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser Ala Ile Val Ile
145          210         215         220
148 Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile Ala Gly Tyr Leu
149 225          230         235         240
152 Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp Lys Lys Thr Lys
153          245         250         255
156 Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe Asp Val Gln Asp
157          260         265         270
160 Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser Lys Asp Lys Pro
161          275         280         285
164 Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu Ile Phe Ser Asp
165          290         295         300
168 Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly Val Asp Thr Asp
169 305          310         315         320
172 Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe Phe Thr Ser Ile
173          325         330         335
176 Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu Ser Asp Leu Tyr

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177          340          345          350
180 Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe Glu Phe Gly Lys
181          355          360          365
184 Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg Phe Val Asp Ile
185          370          375          380
188 Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu Ala Thr Glu Ala
189 385          390          395          400
192 Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr Lys Thr Ile Pro
193          405          410          415
196 Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu Met Pro Asp Lys
197          420          425          430
200 Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu Ile Thr Asp Ile
201          435          440          445
204 Asn Lys Asn
205          450

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208 <210> SEQ ID NO: 3

209 <211> LENGTH: 1263

210 <212> TYPE: DNA

211 <213> ORGANISM: Artificial Sequence

213 <220> FEATURE:

214 <223> OTHER INFORMATION: Description of Artificial Sequence: mhp3 manipulated for in vitro

215 expression

217 <400> SEQUENCE: 3

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218 atgtgggata aagaaacaac taaagaagaa aaatcagccg ataatcaaaa taagcaaadc      60
220 actgatgtct caaaaatttc aggactagtt aatgaacgaa aatccgaaat tatggccgca      120
222 aaagctgatg caaacaaca ttttgggcta aatatggcaa ttgtaaccgc tggtggaacg      180
224 gtaaatgata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt      240
226 actggagggt agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc      300
228 tcaattgcta ataccaacaa aaatgttttg gtactttctg gttttcaaca cggatgatgc      360
230 ttcacaagat gggttaaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc      420
232 atactcgga ttgactggac tgatactgaa aatgtaattc caacaggtcg atatattaat      480
234 ttaacctata aaactgaaga agccggatgg cttgcaggat atgcgaatgc ttcctttttg      540
236 gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tggtgggatt      600
238 tcgccagctg taactgattt tatcgctggg tatctagccg gaattaaagc ttggaatcta      660
240 aaaaattctg ataaaaaaac aaagataaca actgataaaa tcgagataaa tcttggtgtt      720
242 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct      780
244 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcgatat aatcgcaaac      840
246 caaatgatc gttatctcat tgggtgtgac accgaccaat cacttgttta taaaaaaact      900
248 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt      960
250 agtgatttat atacaaaaaa atcaaattca agaaatttag ccggttttga atttggtaaa     1020
252 aaaagtgcaa ccgtttatct tggaattaaa gacagggttg tcgatattgc tgatacttct     1080
254 ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt     1140
256 gaagaaaaaa ctaagacaat tctgcccga gaagttcgta aaactttaga aattccggaa     1200
258 atgcctgata aacaacctga taagcaacag gaaagcttag acaaacttaa ttaccgatat     1260
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263 <210> SEQ ID NO: 4

264 <211> LENGTH: 423

265 <212> TYPE: PRT

266 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING

DATE: 10/26/2004

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Output Set: N:\CRF4\10262004\I676249D.raw

268 <220> FEATURE:

269 <223> OTHER INFORMATION: Description of Artificial Sequence: mhp3 manipulated for in
270 vitro expression

272 <400> SEQUENCE: 4

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278 Asn Lys Gln Ile Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu
279          20          25          30
282 Arg Lys Ser Glu Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe
283          35          40          45
286 Gly Leu Asn Met Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn
287          50          55          60
290 Ser Phe Asn Gln Ser Gly Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu
291 65          70          75          80
294 Thr Gly Gly Glu Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu
295          85          90          95
298 Gly Lys Tyr Ser Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu
299          100         105         110
302 Ser Gly Phe Gln His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro
303          115         120         125
306 Glu Asn Lys Gln Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile
307          130         135         140
310 Asp Trp Thr Asp Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn
311 145          150         155         160
314 Leu Thr Tyr Lys Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn
315          165         170         175
318 Ala Ser Phe Leu Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser
319          180         185         190
322 Ala Ile Val Ile Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile
323          195         200         205
326 Ala Gly Tyr Leu Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp
327          210         215         220
330 Lys Lys Thr Lys Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe
331 225          230         235         240
334 Asp Val Gln Asp Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser
335          245         250         255
338 Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu
339          260         265         270
342 Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly
343          275         280         285
346 Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe
347          290         295         300
350 Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu
351 305          310         315         320
354 Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe
355          325         330         335
358 Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg
359          340         345         350
362 Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu

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363          355          360          365
366 Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr
367          370          375          380
370 Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu
371 385          390          395          400
374 Met Pro Asp Lys Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu
375          405          410          415
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379          420
382 <210> SEQ ID NO: 5
383 <211> LENGTH: 602
384 <212> TYPE: DNA
385 <213> ORGANISM: Mycoplasma hyopneumoniae
387 <400> SEQUENCE: 5
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390 aacgcacac cgtgttgaaa accagaaagt actcaaacat tttgttggt attagcaagt      120
392 gagctatatt ttccttcaag ttcagcagtt gaactatcta ctgaagtaat ctcacctcca      180
394 gtaagagcgc caagttggtg aattgcctct caacttgatt ggtaaataga attatcattt      240
396 accgttccac cagcggttac aattgccata tttagcccaa aatgtttggt tgcacagct      300
398 tttgcggccca taatttcgga ttttcgttca ttaactagtc ctgaaatttt tgagacatca      360
400 gtgatttgct tattttgatt atcggctgat ttttcttctt tagttgtttc tttatcccaa      420
402 catccggcag agattgtcgc gattgctgaa agcggaaaaa ctaagcctaa gccagaagaat      480
404 ttatttcatt ttatcttttt tttcatagtt gttctcctaa ttaattgttt taattacgat      540
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408 ac
411 <210> SEQ ID NO: 6
412 <211> LENGTH: 200
413 <212> TYPE: PRT
414 <213> ORGANISM: Mycoplasma hyopneumoniae
416 <400> SEQUENCE: 6
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423          20          25          30
426 Thr Phe Leu Leu Val Leu Ala Ser Glu Leu Tyr Phe Pro Ser Ser Ser
427          35          40          45
430 Ala Val Glu Leu Ser Thr Glu Val Ile Ser Pro Pro Val Arg Ala Pro
431          50          55          60
434 Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe
435 65          70          75          80
438 Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu
439          85          90          95
442 Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr
443          100          105          110
446 Ser Pro Glu Ile Phe Glu Thr Ser Val Ile Cys Leu Phe Trp Leu Ser
447          115          120          125
450 Ala Asp Phe Ser Ser Leu Val Ser Leu Ser Gln His Pro Ala Glu
451          130          135          140
454 Ile Val Ala Ile Ala Glu Ser Gly Lys Thr Lys Pro Lys Pro Arg Asn

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 3
Seq#:10; N Pos. 9,18,21
Seq#:12; N Pos. 6,9,12,18,21,24
Seq#:14; N Pos. 4,7,10,16,19,22

VERIFICATION SUMMARY

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Input Set : A:\3153.162.PC10555A.Second.Substitute.Seq.10.19.04.ST25.txt

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L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:594 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0